IN THE CLAIMS:

Please cancel claims 6, 8 and 11 without prejudice or disclaimer, amend claims 7 and 10 as follows:

1-6. (Cancelled)

7. (Currently Amended) A method for determining a base sequence of a primer ~~according to Claim 6, further~~ comprising:

carrying out a PCR by using four types of primers which respectively have a structure comprising a first sequence of a given base length complementary to one of single strands of a target DNA and a second sequence of a given base length provided adjacent to the side of 5' terminus of said first sequence and being non-complementary to the one of single strands of the target DNA;

analyzing results of amplified products obtained by the PCR;

requiring efficiencies of adenylation using results of the step of analyzing;

determining one out of the four types of primers as a sequence which is most likely to undergo adenylation, wherein each of the four types of primers have one base at 5' terminus of the second sequence, the one base being different among the four types of primers;

carrying out a second PCR by using another four types of primers which respectively have the one base at the 5' terminus of the second sequence of the sequence determined in the step of determining one out of the four types of primers, and have a second base located at a second site from the 5' terminus thereof and different among the another four types of primers;

analyzing second results of amplified products by the second PCR;

requiring efficiencies of adenylation using results of the step of analyzing the second results; and

determining one out of the another four types of primers to be most likely to undergo adenylation.

8-9. (Cancelled)

10. (Currently Amended) A method for determining a base sequence of a primer ~~according to Claim 7, further~~ comprising: ~~steps of~~

carrying out a PCR by using four types of primers which respectively have a structure comprising a first sequence of a given base length complementary to one of

single strands of a target DNA and a second sequence of a given base length provided adjacent to the side of 5' terminus of said first sequence and being non-complementary to the one of single strands of the target DNA;

analyzing results of amplified products obtained by the PCR;

requiring efficiencies of adenylation using results of the step of analyzing;

determining one out of the four types of primers as a sequence which is most likely to undergo adenylation, wherein each of the four types of primers have one base at 5' terminus of the second sequence, the one base being different among the four types of primers;

carrying out a second PCR by using another four types of primers which respectively have the one base at the 5' terminus of the second sequence of the sequence determined in the step of determining one out of the four types of primers, and have a second base located at a second site from the 5' terminus thereof and different among the another four types of primers;

analyzing second results of amplified products by the second PCR;

requiring efficiencies of adenylation using results of the step of analyzing the second results;

determining one out of the another four types of primers to be most likely to undergo adenylation;

carrying out a third PCR by using other four types of primers which respectively have the one base at the 5' terminus of the second sequence of the sequence determined in the step of determining one out of the another four types of primers, and have a third base located at a third site from the 5' terminus thereof and different among the other four types of primers;

analyzing third results of amplified products obtained by the third PCR;

requiring efficiencies of adenylation using results of the step of analyzing the third results; and

determining one out of the other four types of primers to be most likely to undergo adenylation.

11. (Cancelled)